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Run on:

OM protein - protein search, using sw model

March 18, 2004, 04:07:52; Search time 46 Seconds (without alignments) 2443.187 Million cell updates/sec

2247 1 NDVARGIVKADVAQSSYGLY.....EVQAYNVPVGPQTFSLAIVN 434 US-09-985-689A-1-COPY Title: Perfect score: Seguence:

1049977 seqs, 258955339 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
4: \cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
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11: \cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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	5-689A-1	5-662-2	5-689A-2	5-689A-6	5-689A-7	5-689A-5	5-689A-3	5-689A-4	6-324-10	3-105-13	0-624-12	0-624-1	0-624-4	0 - 624 - 16	2-488-39
	US-09-985-689A-1	US-10-385-662-2	38-60-SC	US-09-985-689A-6	38-60-SC	38-60-SE	186-60-SD	186-60-SD	US-10-33	US-10-40	US-10-09	US-10-09	US-10-09	US-10-09	US-10-11
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ALIGNMENTS

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61 NANDTNGHGTHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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                                                                                                         APPLICANT: HATADA, YUJI
APPLICANT: GCAWA, AKINORI
APPLICANT: GCAWA, AKINORI
APPLICANT: SANGEYAMA, YASUSHI
APPLICANT: SANGEYAMA, YASUSHI
APPLICANT: SANGEYNAMI
APPLICANT: SANTOWN NOWIVEI
APPLICANT: SAEKI, HIROYUKI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: ALKALINE proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR PRILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                      Sequence 1, Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
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RESULT 1
US-09-985-689A-1
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Matches 418; Conservative
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61 NANDINGHGTHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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                                                                                       121 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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Best Local Similarity 99.8%; Pred. No. 5.2e-187;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps
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Sequence 2, Application US/10385662
Sequence 2, Application US/10385662
SEQUENCE CONTROL ON US20040002432A1
GENERAL INFORMATION:
APPLICANT: SATO, TSUVOSHI
APPLICANT: SUNITONO, NOBUVIKI
APPLICANT: SUNITON, NOBUVIKI
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: NOBAYNARI, TORRU
ITLE OF INVENTION: Alkaline protease
FILE REPRESENCE: 23493800
CURRENT PILING DATE: 2003-03-12
FRIOR APPLICATION NUMBER: US/10/385,662
CURRENT FILING DATE: 2003-03-22
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-06-06
FRIOR FILING DATE: 2002-10-18
FRIOR FRIOR DATE: 2002-10-18
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US-10-385-662-2
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121 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPCTAKNAI 180
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121 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI 180
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360 SLTLVNDLDLVITARNGTKKYVGNDFTARYDNNWDGRNNVENVFINARQSGTYTVEVQAYN 419
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                      SVTLVNDLNLVITAPNGTOYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTLEVQAYN 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Score 2120.5; DB 10; Lengt
93.3%; Pred. No. 2.1e-176;
iive 20; Mismatches 8; Indels
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                                                                      421 VPVGPOTFSLAIVN 434
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CRGANISM: Bacillus sp. US-09-985-689A-7
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Matches 405;
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US-09-985-689A-7
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                                                                          361 SVTLVNDLDLVITAPNGTRYVGNDFSAPFDNNWDGRNNVENVFINSPQSGTYTIEVQAYN 420
                                                             PNGNÇGWGRVTLDKSLNVAYVNESSSLSTSÇKATYSFTATAGKPLKISLVWSDAPASTTA 360
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95.1%; Score 2138; DB 10; Length 434;
Best Local Similarity 93.3%; Pred. No. 6.2e-178;
Matches 405; Conservative 20; Mismatches 9; Indels 0
                                                                                                                                                                                                                                VPVGPQTFSLAIVN 434
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ORGANISM: Bacillus sp.
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APPLICANT: KAGEYARA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUNITOMO, NOBUVIKI
APPLICANT: SUNITOMO, NOBUVIKI
APPLICANT: SUNITOMO, NOBUVIKI
APPLICANT: SAEKI, KATSUHISA
TILIB REFERENCE: 212483180
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR PRILING DATE: 2000-11-22
PRIOR PRILING DATE: 2000-11-22
PRIOR PRILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFFWARE: PATENTIN VERSION 3.1
No. US20030022351A1
Publication No. US2003002235
GENERAL INFORMATION:
PAPLICANT: HATADA, VUJI
APPLICANT: OGAWA, AKINORI
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 433
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88.7%; Score 1993.5; DB 10; Length 433;
Best Local Similarity 87.6%; Pred. No. 2.5e-165;
Matches 380; Conservative 29; Mismatches 24; Indels 1;
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: GGAWA, AKINORI
APPLICANT: SAGEXAMA, YASOSHI
APPLICANT: SATO, TSUTYOSHI
APPLICANT: SATO, TSUTYOSHI
APPLICANT: OXUNITONO, NOBUYUKI
APPLICANT: SAEKI, KATSUHISA
TILLE OF INVENTION: ALABINE Proceeses
CURRENT FILLIOR DATE: 2002-07-01
PRIOR PELLING DATE: 2000-11-22
PRIOR FILLING DATE: 2000-11-22
PRIOR FILLING DATE: 2000-11-2
PRIOR FILLING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEDIUM 4.33
                                                                                                                 ; Sequence 5, Application US/09985689A
; Publication No. US20030022351A1
; GENERAL INFORMATION:
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420 VPVSPQTFSLAIVH 433
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                                                                                                                               Gaps
                                                                      Query Match 88.5%; Score 1989.5; DB 10; Length 433; Best Local Similarity 87.3%; Pred. No. 5.7e-165; Matches 379; Conservative 29; Mismatches 25; Indels 1;
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Publication No. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUUI
APPLICANT: OGAWA, AKINORI
APPLICANT: SACEYMAK, YSAUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
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ORGANISM: Bacillus sp.
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                            US-09-985-689A-3
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; Sequence 3, Application US/09985689A

RESULT 7 US-09-985-689A-3

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Score 1581.5; DB 1. Pred. No. 1.7e-129;
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Best Local Similarity 95.3%; Pred. No. ...
Best Local Similarity 95.3%; Mismatches
Matches 303; Conservative 10. Mismatches
Matches 303; Conservative 10. Mismatches
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; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
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Publication No. US20030176304A1

GENERAL INFORMATION:

APPLICANT: Hanean, Peter

APPLICANT: Mikkelsen, Frank

APPLICANT: Mikkelsen, Frank

TITLE OF INVENTION: Procease Variants and Compositions;

FILE REFERENCE: 5349, 204-US

CURRENT APPLICATION NUMBER: US/10/336,324

CURRENT APPLICATION NUMBER: US/09/512,251A

PRIOR FILING DATE: 2003-01-03

PRIOR FILING DATE: 2000-2-24

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%; Score 1982.5; DB 10
llarity 87.1%; Pred. No. 2.3e-164;
Conservative 30; Mismatches 25;
                                    APPLICANT: OKUDA, MITSUYOSHI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
TITLE REPERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR PILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
              SUMITOMO, NOBUYUKI
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US-09-985-689A-4
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Best Local Simi
Matches 378;
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US-10-336-324-10
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208 TVGATENLKPSFGSYADNINHVAQFSSKGPTRDGRIKPDVNAPGTYTLISARSSLAPDSSF 267
241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNARGITPRPSILKAALIAGAADIQGGY 300
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                                                                                                                                                                                                                                                              PANLOTLFSQAYS 147
                                                                                                                                                                                                                                                                                                                  SAPGTAKNAI 180
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                                                                                                  GOGGIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN
                                                                                                                                             (GOGOIVAVADIGLDIGRNDSSMHEAFRGKITALYALGRIN
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APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Manden, Frank
TITLE OF INVENTION: Procease Variants And Compositions
FILE REFERENCE: 5435.200-US
CURRENT PELLING DATE: 2003-031
PRIOR APPLICATION NUMBER: US/10/403, 105
PRIOR APPLICATION NUMBER: US/09/196, 281A
PRIOR FILING DATE: 1998-11-19
PRIOR FILING DATE: BARLIER PILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
: ENGITE: 345
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70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1.7e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1;
                                                 4; Indels
                                                                                                                                                                                                          NKGMAPQANLVPQSIMDSGGGLGGLF
                                                                                                                                                                                                                                                                                                                     AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNG
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72 VAGSVIGNGSTN----KGMAPQANIVFQSIM--DSGGGLGGLPSNLQTLFSQAYSAGARI 125
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18.2%; Score 409; DB 13; Length 412;
Best Local Similarity 29.6%; Pred. No. 4.6e-27;
Matches 135; Conservative 60; Mismatches 147; Indels 114;
                                                                                                                                                                                                                                Sequence 1, Application US/1009624

publication No. US20020132335A1

GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SANDA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANTON NUMBER: 09/45,472
PRIOR FILING DATE: 1999-120-06
PRIOR FILING DATE: 1999-120-06
PRIOR FILING DATE: 1999-120-06
PRIOR FILING DATE: 1999-100-06
PRIOR FILING DATE: 1999-100-06
NUMBER OF SEQ ID NOS: 33
SOCTUMBER: Patentin version 3.0
SEQ ID NO 1

FUNDALLY
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                                      501 --GFEKVGYYNPTAGTWTVKVVSYK---GAANYQVDVVS 534
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396 RNNVENVFINAPOSGTYTIEVQAYNVPVGPOTFSLALVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 412
TYPE: PRT
COGGANISM: Pyrococcus furiosus
US-10-090-624-1
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   148 AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 207
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APPLICANT: TAKAKURA, Hikaru
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
ITLE OF INVENTION: SYSTEM FOR EXPRESSING HYP
FILE REFERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-16-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PARENTI NOS: 33
LENGTH: 659
LENGTH: 659
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US-10-090-624-12
Sequence 12, Application US/10090624
Publication No. US20020132335A1
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Best Local Similarity 29.89
Matches 137; Conservative
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399 VENVFINAPQSGTYTIEVOAYNVPVGPQTFSLAIVN 434
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           CURRENT APPLICATION NUMBER: US/10/090,6:
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR PILING DATE: 1997-06-10
NUMBER OF SEO ID NOS: 33
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                ORGANISM: Pyrococcus furiosus
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35; Conservative
FILE REFERENCE: TAKAKURA=6
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US-10-112-488-39
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Matches 135;
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18.2%; Score 409; DB 13; Length 522;
Best Local Similarity 29.6%; Pred. No. 6.6e-27;
Matches 135; Conservative 60; Mismatches 147; Indels 114; Gaps
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                                            APPLICANT: ASADA, KIJOZO
APPLICANT: KATO, ILOMOSAIA
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKANCHR=6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATEURIUM VETSION 3.0
SEQ ID NO 4
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APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: AFOYO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa at position 428 is Gly or Val. US-10-090-624-4
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                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pyrococcus furiosus
                                          Tomoko
  TAKAKURA, Hikaru
                        MORISHITA, Mio
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (428) . (428)
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                                     SHIMOJO,
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203 VASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVEWAVDNKDKYGIKV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 INLSLGSSQSSDGTDALSQAVNAAWDA------GLVVVVAAGNSGPNKYTIGSP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 ---GTSMGQPINDYYTAAPGTSMATPHVAGIAALLLQ-----AHPSWTPDKVKTALIB 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GA-----ADIGLGYPNGNQGWGRVTLDKSLNVAYVNESSSLSTSOKA----TYSFT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADIVKPDEIADIAYGA-----GRVNAYKAIN--YDNYAKLVFTGYVANKGSQTHQFV 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 ATAGKPLKISLVWSDAPASTTASVTLVNDLNLVITAPNGTQYVGNDFTSPYNDNWDGRNN 398
                                                                                                                                                                                                                                                            72 VAGSVLGNGSTN----KGMAPQANLVFQSIM--DSGGGLGGLPSNLQTLFSQAYSAGARI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 LAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPK--PSLLKAALIA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 ISGASFVTATLYWDNAN-----SDLDLYLYDPNGNQ-VDYSYTAYY-----G 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 HTNSWGA------AVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 GTAKNAITVGATENLRPSFGSYADNINHVAOFSSRGPTKDGRIKPDVMAPGTFILSARSS
                                                                                                                                                                           18 GLYGQGQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRINNAN------DTNGHGTH
                                                                  Gaps
18.2%; Score 409; DB 13; Length 654;
29.6%; Pred. No. 9.1e-27;
tive 60; Mismatches 147; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DATE, MESAYO
APPLICANT: UNEXAMA, YUKLKO
APPLICANT: WATSUI Hiroshi
ITILE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
FILE REFERENCE: 1928640500NT
CURRENT PELING DATE: 2002-04-01
PRIOR PELING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: DET/JPD0/06780
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 1909-09-30
NUMBER OF SEQ ID NOS: 70
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220 VMAPGTFILSARSSLAPDSSFWANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGIT 279
                                                                                                                                                                                                                                                                                                                                                                                                                280 PKPSLIKAALIAGAADIGLG-YPNGNQGWGRVTLDKSLNVAYVNESSSLS----- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ---TSQKATYSFTATAGKPLKISLVMSD----APAS--TTASVTLVNDLNLVITAP-NG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GGLPSNLQTLFSQAYSAGARIHTNSWGAAVNGAYTTDSRNVDDYVRK--NDMTLF--AA 160
                                                                                                                                                                                                                                                                                                272 FGDDSGILAGMEWAAAQGADIVNMSLG----GMDTPETDPLEAAVDKLSAEKGILFAIAA 327
                                                                                                                                                                                                                                                                                                                                     161 GNEGPNGGTISAPGTAKNAITVGATENLRPSFGSYADNINHVAQFSSRGP-TKDGRIKPD 219
                                                                                                                                                                                                                                                                                                                                                        49 KITALYALGRINNANDINGHGTHVAGSVLGNGS----TNKGMAPQANLVFQSIMDSGGGL 104
                                                                                                                                                                                                                                      3 VAR----GIVKADVAQS-----SYGLYGQGQIVAVADTGLDTGRNDSSMHEAFRG 48
                                                                                                                                 Gaps
                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 16.3%; Score 366; DB 14; Length 1079; Best Local Similarity 31.6%; Pred. No. 1.1e-22; Matches 148; Conservative 55; Mismatches 175; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOYVGNDFTSPYNDNWDGRNNVENVFINAPOS----GTYTIEVQAYNV 421
                                        ; TYPE: PRT ; ORGANISM: Streptomyces albogriseolus US-10-112-488-39
; SOFTWARE: Patentin version 3.1; SEQ ID NO 39; LENGTH: 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378
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Search completed: March 18, 2004, 04:12:40 Job time: 47 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

March 18, 2004, 04:07:52; Search time 46 Seconds Run on:

OM protein - protein search, using sw model

(without alignments) 2443.187 Million cell updates/sec

US-09-985-689A-1-COPY 2247 1 NDVARGIVKADVAQSSYGLY......EVQAYNVPVGPQTFSLAIVN 434 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1049977 seqs, 258955339 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1. /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2. cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USOO_NEW_PUB.pep:* . cgn2_6/prodata/2/pubpaa/USO9E PUBCOMB.pep: . cgn2_6/prodata/2/pubpaa/USO9E PUBCOMB.pep: . cgn2_6/prodata/2/pubpaa/USO9C_PUBCOMB.pep: . cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep: . cgn2_6/prodata/2/pubpaa/USOO_NEW_PUB.pep: .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Seguence 6, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 13, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 39, Appl
SUMMARIES			OH	US-09-985-689A-1	US-10-385-662-2	US-09-985-689A-2	US-09-985-689A-6	US-09-985-689A-7	US-09-985-689A-5	US-09-985-689A-3	US-09-985-689A-4	US-10-336-324-10	US-10-403-105-13	US-10-090-624-12	US-10-090-624-1	US-10-090-624-4	US-10-090-624-16	US-10-112-488-39
			98	10	13	10	10	10	10	10	10	14	74	13	13	13	13	14
			Match Length DB	434	434	434	434	433	433	433	433	345	345	629	412	522	654	1079
	₩	Query	Match	8.66	8.66	97.3	95.1	94.4	88.7	88.5	88.2	70.4	70.4	19.9	18.2	18.2	18.2	16.3
			Score	2242	2242	2186	2138	2120.5	1993.5	1989.5	1982.5	1581.5	1581.5	447.5	409	409	409	366
		Result	No.	н	7	m	4	ហ	9	7	œ	ത	10	F	12	13	14	15

Sequence 13251, A Sequence 10856, A Sequence 10856, A Sequence 114, Appli Sequence 59, Appli Sequence 59, Appli Sequence 25271, Sequence 25271, Sequence 25271, Sequence 25271, Sequence 5, Appli Sequence 6, Appli Sequence 50, Appli Sequence 60, App	10, 10, 16,
US	US-10/242-349-44 US-10/242-549-15 US-08-322-678-16 US-09-837-235-16 US-09-060-8548-6 US-09-975-139-1
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ALIGNMENTS

CRGANISM: Bacillus sp. US-09-985-689A-1 RESULT 1 US-09-985-689A-1

ô Length 434; Indels 99.8%; Score 2242; DB 10; ilarity 99.8%; Pred. No. 5.2e-187; Conservative 1; Mismatches 0; Similarity 433; Query Match Best Local S Matches 433

1 NDVARGIVKADVAQSSYGLYQQQQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRIN 60 1 NDVARGIVKADVAQSSYGLYGQQQIVAVADTGLDTGRNDSSMHEAFRGKITALYALGRTN 60 g

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61 NANDTNGHGTHVAGSVLGNGSTNKCMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120

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                                                                                                                                                  181 TVGATENLRPSFGSYADNINHVAQFSSRGPTXDGRIXPDVMAPGTFILSARSSLAPDSSF
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                                                                                                                                                                                                            241 WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
                                                                                                                                                                                                                                                 301 PNGNQGWGRVTLDXSLNVAYVNESSSLSTSQXATYSFTATAGKPLKISLVWSDAPASTTA
                                              121 AGARIHTNSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI
                                                                                                    181 TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
121 AGARIHTWSWGAAVWGAYTTDSRNVDDYVRKNDWTILFAAGNEGPWGGTISAPGTAKWAI
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96.3%; Pred. No. 4e-182;
iive 14; Mismatches 2;
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APPLICANT: GAGWA, AKINGNI
APPLICANT: GAGWA, KINGNI
APPLICANT: GAGNA, KINGNI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: STRAKI, KATSUHKAI
APPLICANT: ONUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: UP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SEQ TWARRE: PATCHTIN VERSION 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09985689A, publication No. US20030022351A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPVGPQTFSLAIVN 434
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Best Local Similarity 96.3%
Matches 418; Conservative
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ORGANISM: Bacillus sp.
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US-09-985-689A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLVNDLNLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVILVNDLDLVITAPNGTQYVGNDFTSPYNDNWDGRNNVENVFINAPQSGTYTIEVQAYN 420
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     TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
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                                                                                                                           AGARIHTINSWGAAVNGAYTTDSRNVDDYVRKNDMTILFAAGNSGPNGGTISAPGTAKNAI
                                                                                                                                                                                             TVGATENLRPSFGSYADNINHVAQFSSRGPTKDGRIKPDVMAPGTFILSARSSLAPDSSF
                                                                                      AGARIHINSWGAAVNGAYITDSRNVDDYVRKNDMTILFAAGNEGPNGGTISAPGTAKNAI
                                                                                                                                                                                                                                                                                                     WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
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Sequence 2, Application US/10385662

PUblication No. US20040002432A1

GENERAL INFORMATION:

APPLICANT: OKUDA, MITSTYCSHI

APPLICANT: SATO, TSUXOSHI

APPLICANT: SATO, TSUXOSHI

APPLICANT: SATO, TSUXOSHI

APPLICANT: SUMITOMO, NOBUVUKI

APPLICANT: SUMITOMO, NOBUVUKI

APPLICANT: SUMITOMO, NOBUVUKI

APPLICANT: SAEKI, KATSUHISA

APPLICANT: LZAMA, YOSHIFUMI

APPLICANT: NOMURA, MASAFUMI

TITLE OF INVENTION: AIABINE protease

FILE REFERENCE: 234938USO

CURRENT FILING DATE: 2003-03-12

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-06-06

PRIOR FILING DATE: 2002-10-18

PRIOR FILING DATE: 2002-10-18
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CRGANISM: Bacillus sp. KSM-KP43
US-10-385-662-2
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                                                                  361 SVILVNDLDLVITAPNGTKYYGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAXN 420
301 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA 360
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                                                                                                                                                                                                                                                                                                                                   GEREKAL INFOGRATION:
APPLICANT: GGAMA, AKINORI
APPLICANT: GGAMA, AKINORI
APPLICANT: SAGEYAMA, YAGUSHI
APPLICANT: SAGEYAMA, YAGUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: GWUTOWO, NOBUYUKI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: ALKALINE proteases
FILE REFERENCE: 215483180
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT PILING DATE: 2002-07-01
PRIOR PRILIAGION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                          ; Sequence 7, Application US/09985689A
; Publication No. US20030022351A1
; GENERAL INFORMATION:
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; ORGANISM: Bacillus sp.
US-09-985-689A-7
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                                                      241 WANHDSKYAYMGGISMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADVGLGY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HATADA, YUJI
APPLICANT: GGAWA, AKINORI
APPLICANT: GGAMA, AKINORI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: OKUNITONO, NOBUYUKI
APPLICANT: SAEKI, KATSUTISA
TITLE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6 Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 VPVGPQTFSLAIVN 434
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Best Local Similarity 93.3
Matches 405; Conservative
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ORGANISM: Bacillus sp
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US-09-985-689A-6
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Publication No. US20030022351A1 GENERAL INFORMATION:
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87.6%; Pred. No. 2.5e-165;
tive 29; Mismatches 24; Indels
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APPLICANT: GGAWA, AKINORI
APPLICANT: GGAWA, AKINORI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SAGEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
APPLICANT: STUNTOWO, NOBUTUKI
APPLICANT: SAEXI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
FILE REFERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
FENDRY ARABITAND AND ASSIONAL ASSIONA
                                                                                                                                                                                                      ; Sequence 5, Application US/09985689A; Publication No. US20030022351A1; GENERAL INFORMATION:
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                 VPVSPQTFSLAIVH 433
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Matches 380, Conservative
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Best Local ?
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61 NANDTNGHGTHVAGGYLGNGSTNKGNAPQANLVFQSIMDSGGGLGGLFSNLQTLFSQAYS 120
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88.5%; Score 1989.5; DB 10; Lengtl
Best Local Similarity 87.3%; Pred. No. 5.7e-165;
Matches 379; Conservative 29; Mismatches 25; Indels
GENERAL INFOCATION:
APPLICANT: GCAWA, YUJI
APPLICANT: GCAWA, AKINORI
APPLICANT: SACEYAMA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAXI, HIROYUKI
APPLICANT: ARAXI, HIROYUKI
APPLICANT: ARAXI, KATSUHISA
TITLE OF INVENTION: AIRAILINE PROCESSES
TITLE OF INVENTION: AIRAILINE PROCESSES
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENT NOS: 7
SOFTWARE: PATENT NOS: 7
SEQ ID NO 3:
ENGINE ASSA
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Publication No. US20030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: OGAWA, AKINORI
APPLICANT: SAGRYAMA, YSSUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: ARAKI, HIROYUKI
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179 240 360

; Sequence 3, Application US/09985689A

RESULT 7 US-09-985-689A-3

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61 NANDINGHGIHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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87.1%; Pred. No. 2.3e-164;
wiematches 25; Indels
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APPLICANT: Bauditz, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349.204-US
CURRENT APPLICATION NUMBER: US/10/336,324
CURRENT PILING DATE: 2003-01-03
FRIOR PEDITOR TOWNER: US/09/512,251A
FRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ. ID NOS: 12
SOFTWARE: Patentin version 3.1
               APPLICANT: OKUDA, MITSUYOSHIA
APPLICANT: SAEKT, KATSUHISA
APPLICANT: SAEKT, KATSUHISA
APPLICANT: SAEKT, KATSUHISA
FILE REPERENCE: 215483USO
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: UP P2000-355166
PRIOR PILING DATE: 2000-11-22
PRIOR PPLICATION NUMBER: UP P2001-114048
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SENGTH: 433
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SUMITOMO, NOBUYUKI
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Best Local Similarity
Matches 378; Conservat
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US-10-336-324-10
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US-09-985-689A-4
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APPLICANT:
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40 41

61 NANDTRGHGTHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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181 TVGATENLRPSFGSYADNINHVAQFSSRGPPKDGRIKPDVMAPGTFTILSARSSLAPDSSF 240
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Publication No. US20330180933A1
GENERAL INFORMATION: Peter K.
APPLICANT: Hansen, Peter K.
APPLICANT: Banditz, Peter
APPLICANT: Banditz, Peter
TITLE OF INVENTION: Protease Variants And Compositions
FILE REFRENCE: 5435,200,US
CURRENT APPLICATION NUMBER: US/10/403,105
CURRENT APPLICATION NUMBER: US/09/196,281A
PRIOR FILING DATE: 1998-11-19
PRIOR FILING DATE: 1998-11-19
PRIOR FILING DATE: BARLIER FILING DATE: 1932/97
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70.4%; Score 1581.5; DB 14; Length 345;
Best Local Similarity 95.3%; Pred. No. 1.7e-129;
Matches 303; Conservative 10; Mismatches 4; Indels 1:
                                                                                                                                     70.4%; Score 1581.5; DB 14; Length 345; 95.3%; Pred. No. 1.7e-129; ative 10: Mismatches 4; Indels 1; M/10/17
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12. AGARIHINSHGAAVNGAYITDSRNVDDYVRKNDMILLFAAGNEGPNGGII
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SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Bacillus
10-403-105-13
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                                                                                                                                                                                                                            1 NDVARGIVKADVAQSSYGL
                                                                                                                                                                              Matches 303; Conservative
                                                                                                                                                             Similarity
                                               TYPE: PRT
CORGANISM: Bacillus
US-10-336-324-10
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LENGTH: 345
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396 RNNVENVFINAPOSGTYTIEVQAYNVPVGPQTFSLAIVN 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 GHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKY 258
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                                                                    267
                                                                                                                       WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY 300
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   AGARIHINSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI
                                                                  TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIKPDVMAPGTYILSARSSLAPDSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.9%; Score 447.5; DB 13; Length llarity 29.8%; Pred. No. 4e-30; Conservative 68; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10090624 Publication No. US20020132335Al GENERAL INFORMATION:
                                                                                                                                                                        PNGNOGWGRVTLDKSLNV 318
                                                                                                                                                                                                      PNGNGGWGRVTLDKSLNV 345
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ORGANISM: Thermococcus celer
                                                                                                                                                                                                                                                                                                                                         APPLICANT: TAKAKURA, Hikaru
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Best Local Similarity
Matches 137; Conserv
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US-10-090-624-12
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292 GA-----ADIGLGYPNGNQGWGRVTLDKSLNVAYVNESSSLSTSQKA----TYSFT 338
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18.2%; Score 409; DB 13; Length 412;
Best Local Similarity 29.6%; Pred. No. 4.6e-27;
Matches 135; Conservative 60; Mismatches 147; Indels 114; Gaps
                                                                                                                                                                                                                                                                        APPLICANT: ADALAGAM, MARAGAM MORISHTA, Michael APPLICANT: SHIMOJO, Tomoko APPLICANT: SHIMOJO, Tomoko APPLICANT: SHADA, Kiyozo APPLICANT: KATO, Tkunoshin TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE FILE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE CURRENT APPLICATION NUMBER: US/10/090,624 CURRENT APPLICATION NUMBER: 05/0445,472 PRIOR APPLICATION NUMBER: 05/0445,472 PRIOR APPLICATION NUMBER: 15/069/1997 PRIOR PLING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 NUMBER OF SEQ ID NOS: 33 SOFTWARE: PATENTIN VERSION 3.0
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399 VENVFINAPOSGTYTIEVQAYNVPVGPQTFSLAIVN 434
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, Sequence 4, Application US/10090624
; Publication No. US20020132335A1
; GENERAL INFORMATION:
                                                                                                                                                                 Sequence 1, Application US/10090624 Publication No. US20020132335A1 GENERAL INFORMATION:
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US-10-090-624-1
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US-10-112-488-39
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ORGANISM:
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18.2%; Score 409; DB 13; Length 522;
Best Local Similarity 29.6%; Pred. No. 6.6e-27;
Matches 135; Conservative 60; Mismatches 147; Indels 114; Gaps
APPLICANT: ASADA, VINCORO, APPLICANT: ASADA, VINCORO);
APPLICANT: ASADA, VINCORDI
JATLICANT: ASADA, SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAURALe
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 1090-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER: OF SEQ ID NOS: 33
SOFTWARE: PALCHLIN VORS: 33
SEQ ID NO 4
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APPLICANT: ASADA, KAYOZO
APPLICANT: KAYOZO
APPLICANT: KAYOZO
APPLICANT: KAYOZO
APPLICANT: KAYOZO
APPLICANT: KAYOZO
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
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LOCATION: (428)..(428)
OTHER INFORMATION: Xaa at position 428 is Gly or Val.
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US-10-090-624-16
; Sequence 16, Application US/10090624
; Fublication No. US20020132335A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pyrococcus furiosus
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SHIMOJO, Tomoko
ASADA, Kiyozo
KATO, Ikunoshin
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APPLICANT: MORISHITA, Mio
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72 VAGSVLGNGSTN----KGMAPQANLVFQSIM--DSGGGLGGLPSNLQTLFSQAYSAGARI 125
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18.2%; Score 409; DB 13; Length 654;
Best Local Similarity 29.6%; Pred. No. 9.1e-27;
Matches 135; Conservative 60; Mismatches 147; Indels 114;
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APPLICANT: UMEZAWA, Yukiko
APPLICANT: UMEZAWA, Keitchi
APPLICANT: VOXOXAMA, Keitchi
APPLICANT: MATSUI, Hiroshi
FITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE
FILE REFERENCE: 219286USSOCNT
CURRENT APPLICATION NUMBER: US/10/112,488
CURRENT APPLICATION NUMBER: DCT/JD00/06780
PRIOR APPLICANT UNIMBER: PCT/JD00/06780
PRIOR PLILING DATE: 2000-09-29
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LICATION NUMBER: US/10/090,624
                      CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 16
LENGTH: 654
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PRIOR APPLICATION NUMBER: JP2000-280098
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PRIOR APPLICATION NUMBER: JP11-280098
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 70
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                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pyrococcus furiosus
US-10-090-624-16
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                                                                                                                                                                                                                   KITALYALGRINNANDINGHGTHVAGSVLGNGS----INKGMAPQANLVFQSIMDSGGGL 104
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                                                                                                                      Query Match
Best Local Similarity 31.6%; Pred. No. 1.1e-22;
Matches 148; Conservative 55; Mismatches 175; Indels 90
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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Streptomyces albogriseolus
US-10-112-488-39
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Search completed: March 18, 2004, 04:12:40 Job time : 47 secs

Sequence 4, Appli Sequence 5, Appli Sequence 55, Appl Sequence 59, Appl Sequence 2, Appli Sequence 12934, A

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Sequence Sequence

Sequence 58, Apr Sequence 10, Appl Sequence 16, Appl Sequence 6, Appli Sequence 1, Appli

Sequence Sequence Sequence

4, Appli 114, App 4, Appli 6, Appli

Sequence

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61 NANDTNGHGTHVAGSVLGNGSTNKGMAPQANLVFQSIMDSGGGLGGLPSNLQTLFSQAYS 120
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4 US-10-156-761-13251

4 US-10-156-761-10856

4 US-10-344-657-4

5 US-10-084-846A-14

5 US-10-084-846A-4

10 US-09-927-827-55

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10 US-09-927-827-59

10 US-09-927-934A-5

10 US-09-13-408-6

10 US-09-813-408-6

10 US-09-927-849-54

10 US-10-242-549-54

10 US-10-242-549-64

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100.0%; Score 2247; DB 10;
Best Local Similarity 100.0%; Pred. No. 8.2e-188;
Matches 434; Conservative 0; Mismatches 0;
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US-09-837-235-16
US-09-060-854B-6
US-09-975-139-1
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APPLICANT: GARAA, YUUI
APPLICANT: GARGEYAMA, YANDRI
APPLICANT: SACGEYAMA, YANDRI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SUNITOWN NOBUVKI
APPLICANT: SUNITOWN NOBUVKI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: ALRAINE PROCESSES
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 2000-11-2
PRIOR FILING DATE: 2000-11-2
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
LENGHREE: PALENTIN VERSION 3.1
SEG ID NO 1
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; ORGANISM: Bacillus sp.
US-09-985-689A-1
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                                                                                                                                                                                                                  March 18, 2004, 04:07:02; Search time 45 Seconds (without alignments) 2497.480 Million cell updates/sec
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2247
1 NDVARGIVKADVAQSSYGLY......EVQAYNVPVGPQTFSLAIVN 434
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/PCTUS_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-985-689A-6
US-09-985-689A-7
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US-09-985-689A-4
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US-10-090-624-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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US-09-985-689A-
US-09-985-689A-
Publication No. US2030022351A1
GENERAL INFORMATION:
APPLICANT: HATADA, YUJI
APPLICANT: GGMAA, AKINORI
APPLICANT: GGMAA, YASUSHI
APPLICANT: SATO, TSUTOSHI
APPLICANT: SATO, TSUTOSHI
APPLICANT: SATO, TSUTOSHI
APPLICANT: SUMITOMO, NOBUVUKI
APPLICANT: SUMITOMO, NOBUVUKI
APPLICANT: STARKI, MARSUNIA
APPLICANT: STARKI, ARTSUTOSHI
APPLICANT: STARKI, ARTSUTOSHI
APPLICANT: SASKI, KATSUHISA
TILE REFERENCE: 215-483US0
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-07-01
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2: 7
SEQ ID NO 2: 7
SED TENDER PATENTIN VERSEN IN SEQ ID NOS: 7
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APPLICANT: SATO, ISUYOSHI
APPLICANT: SATO, ISUYOSHI
APPLICANT: SATO, ISUYOSHI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: IZAWA, YOSHIFUMI
APPLICANT: SAEKI, KARSUHISA
APPLICANT: KOBAYASHI, TOHRU
ITILE OF INVENTION: ALKAINESA
APPLICANT: NOWURA, MASAFUMI
ITILE OF INVENTION: ALKAINE BIOCEASE
CURRENT APPLICATION NUMBER: US 1002-03-12
PRIOR APPLICATION NUMBER: JP 2002-165987
PRIOR FILING DATE: 2003-06-06
PRIOR PILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-10-18
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Publication No. US20040002432A1
GENERAL INFORMATION:
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US-10-385-662-2
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361 SVILVNDLDLVITAPNGTKYVGNDFTAPYDNNWDGRNNVENVFINAPQSGTYTVEVQAYN 420
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301 PSGNQGWGRVTLDKSLNVAFVNETSSLSTNQKATYSFTAQSGKPLKISLVWSDAPASTSA 360
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GARMA, YUUI
APPLICANT: GAGENAM, YUUI
APPLICANT: GAGENAM, YENORI
APPLICANT: GAGENAM, YESUSHI
APPLICANT: SATO, TSUYGHI
APPLICANT: SATO, TSUYGHI
APPLICANT: SUNTOWO, NOBUYUKI
APPLICANT: SAEKI, HIROYUKI
APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: AIARINE PROCESSES
TITLE REPERENCE: 212483130
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: JP P2000-355166
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
NUMBER: OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.1 SEQ ID NO 7 LENGTH: 433
                                                                                                                                          421 VPVGPOTFSLAIVN 434
                                                                                                                                                                     121 VPQGPQAFSLAIVN 434
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US-09-985-689A-7
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US-09-985-689A-7
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                                                                                                                                                 301 PNGNQGWGRVTLDKSLNVAXYNESSALSTSQKATYTFTATAGKPLKISLVWSDAPASTTA
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                           WANHDSKYAYMGGTSMATPIVAGNVAQLREHFVKNRGITPKPSLLKAALIAGAADIGLGY
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95.4%; Score 2143; DB 10; Length 434;
Best Local Similarity 93.5%; Pred. No. 1e-178;
Matches 406; Conservative 19; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SAEKI, KATSUHISA
TITLE OF INVENTION: Alkaline proteases
TILLE OF INVENTION: Alkaline proteases
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT APPLICATION NUMBER: US/09/985,689A
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: JP P2000-355166
PRIOR APPLICATION NUMBER: JP P2001-114048
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09985689A Publication No. US20030022351A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HATADA, YUJI
APPLICANT: GGAWA, AKINORI
APPLICANT: KAGESAWA, YASUSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SARXI, HIROYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: SUMITOMO, NOBUYUKI
APPLICANT: SAEKI, KATSUHISA
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; ORGANISM: Bacillus sp.
US-09-985-689A-6
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396 RNNVENVFINAPQSGTYTIEVQAYNVPVGPQTFSLAIVN 434
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Publication No. US20020132335Al
GENERAL INFORMATION:
                                                                                                                    Sequence 1, Application US/10090624
Publication No. US20020132335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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                                                                                    RESULT 12
US-10-090-624-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 GIRVINLSLGSSQSSDGTDSLSQAVNNAMDA------GIVVCVAAGNSGPNTYT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 AALIAGA-----ADIGLGYPNGNQGWGRVTLDKSL---NVAYVNESSSLSTSQKATY 335
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                                                               TVGATENLRPSFGSYADNINHVAQFSSRGPTRDGRIXPDVMAPGTYILSARSSLAPDSSF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 TALIETADIVAPKEIADIAYGA-----GRVNVYKAIKYDDYAKUTFTGSVADKGSATH 457
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AGARIHTNSWGAPVNGAYTTDSRNVDDYVRKNDMTILFAAGNEGPGSGTISAPGTAKNAI 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Mismatches 153; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 659;
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERENCE: TAKAKURA=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
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20.1%; Score 452.5; DB 1
Best Local Similarity 30.1%; Pred. No. 1.3e-30;
Matches 138; Conservative 67; Mismatches 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DAPE: 2002-03-06
PRIOR PPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION WHORE: 151969/1997
PRIOR APPLICATION WHORE: 151969/1997
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 659
                                                                                                                                                                                                                                                                                             Sequence 12, Application US/10090624
Publication No. US20020132335A1
                                                                                                                                                                                                 PNGNQGWGRVTLDKSLNV 345
                                                                                                                                                                        PNGNQGWGRVTLDKSLNV 318
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ORGANISM: Thermococcus celer
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                                                                                                                                                                                                                                                                                          APPLICANT: TAZAKUTA,
APPLICANT: MORISHITA, Mio
APPLICANT: MERINO, Tomoko
APPLICANT: STEMOLO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2002-03-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-06-10
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18.4%; Score 414; DB 13; Length 412;
Best Local Similarity 29.8%; Pred. No. 1.5e-27;
Matches 136; Conservative 59; Mismatches 147; Indels 11.
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501 --GFEKVGYYNPTAGTWTVKVVSYK---GAAANYQVDVVS 534
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REFERENCE: TAKAKURA=6
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US-10-112-488-39
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18.4%; Score 414; DB 13; Length 522;
Best Local Similarity 29.8%; Pred. No. 2.1e-27;
Matches 136; Conservative 59; Mismatches 147; Indels 114; Gaps
         APPLICANT: MORISHITA, Mio

APPLICANT: SALMOJO, Tomoko

APPLICANT: SEHTWOJO, Tomoko

APPLICANT: ASADA, KIYOZO

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 151969/1997

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOSTWARE: Patentin Version 3.0

SEQ ID NOS
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APPLICANT: MORISHITA, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
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Publication No. US20020132335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature LOCATION: (428)..(428)
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US-10-090-624-16
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2.9e-27;
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CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1999-12-06
PRIOR PELING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 654
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18.4%; Score 414;
Best Local Similarity 29.8%; Pred. No. 2
Matches 136; Conservative 59; Mismatch
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Publication No. US20030082746A1
                                                                                                                                                                                                                                                                                                                          TYPE: PRT : ORGANISM: Pyrococcus furiosus US-10-090-624-16
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APPLICANT: KIKUCHI, Yoshimi
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                                                                                                                                                                                                                                         49 KITALYALGRINNANDINGHGTHVAGSVLGNGS----TNKGMAPQANLVFQSIMDSGGGL 104
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                                                                                                                                                                                                                                                                                                                 214 QVTASKONFTSAPTTGDVVGHGTHVASIAAGTGAQSKGTXKGVAPGAKILNGKVLDDAG-- 271
                                                                                                                                                                                                                                                                                                                                                                        105 GGLPSNLQTLFSQAYSAGARIHTNSWGAAVNGAYTTDSRNVDDYVRK--NDMTILF--AA 160
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                                                    TYPE: PRT / ORGANISM: Streptomyces albogriseolus US-10-112-488-39
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